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OM nucleic - nucleic search, using sw model

Run on: October 23, 2003, 18:15:42 ; Search time 4096 Seconds
                                             (without alignments)
                                             12905.819 Million cell updates/sec

Title: US-09-864-464-9
Perfect score: 2175
Sequence: 1 acttgagcctccaccttctc..........aattggtgcttttgatagcc 2175

Scoring table: IDENTITY NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1: em_estba:*
                 2: em_esthum:*
                 3: em_estin:*
                 4: em_estmu:*
                 5: em_estov:*
                 6: em_estpl:*
                 7: em_estro:*
                 8: em_htc:*
                 9: gb_est1:*
                 10: gb_est2:*
                 11: gb_htc:*
                 12: gb_est3:*
                 13: gb_est4:*
                 14: gb_est5:*
                 15: em_estfun:*
                 16: em_estom:*
                 17: em_gss_hum:*
                 18: em_gss_inv:*
                 19: em_gss_pln:*
                 20: em_gss_vrt:*
                 21: em_gss_fun:*
                 22: em_gss_mam:*
                 23: em_gss_mus:*
                 24: em_gss_pro:*
                 25: em_gss_rod:*
                 26: em_gss_phg:*
                 27: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2175	100.0	2220	11	AY103979	AY103979 Zea mays
c	2	772.6	35.5	916	14	CD446565	CD446565 EL01T0203
	3	758.2	34.9	771	14	CD445806	CD445806 EL01T0203
	4	757.8	34.8	776	14	CD432929	CD432929 EL01N0302
c	5	606	27.9	606	10	AW927326	AW927326 945008H12
c	6	606	27.9	639	9	AI461527	AI461527 486018G03
c	7	583.6	26.8	631	14	CA401911	CA401911 EL01N0428
	8	583.4	26.8	601	14	CD443593	CD443593 EL01N0428
	9	579	26.6	631	9	AW066125	AW066125 687006E08
	10	559	25.7	559	9	AW787460	AW787460 945008H12
	11	555	25.5	555	9	AW787459	AW787459 945008H12
	12	546.4	25.1	860	14	CB627677	CB627677 OSIIEb02M
	13	539.4	24.8	1963	11	AK089053	AK089053 Mus muscu
	14	538	24.7	1960	11	BC013246	BC013246 Homo sapi
	15	537.8	24.7	1963	11	AK090203	AK090203 Mus muscu
c	16	537.6	24.7	544	10	BE644368	BE644368 946060C10
c	17	522.6	24.0	535	9	AI615210	AI615210 486094F05
	18	521.8	24.0	663	12	BJ549326	BJ549326 BJ549326
c	19	520	23.9	553	12	BQ060151	BQ060151 952038D12
	20	511.2	23.5	684	10	BE585724	BE585724 Est#1SP6
	21	509.2	23.4	525	13	BU037922	BU037922 946143C06
	22	499.6	23.0	576	10	BE596995	BE596995 PI1_60_A1
	23	499.4	23.0	512	10	BE511408	BE511408 946060C10
	24	498.8	22.9	582	10	BE596913	BE596913 PI1_60_A1
	25	493	22.7	659	14	CD234175	CD234175 SS1_6_E12
	26	490.6	22.6	650	14	CA741660	CA741660 wialc.pk0
	27	471.6	21.7	614	12	BJ551241	BJ551241 BJ551241
	28	465	21.4	465	9	AW787461	AW787461 945008H12
	29	459.8	21.1	632	9	AV833455	AV833455 AV833455
	30	458.2	21.1	590	12	BJ257506	BJ257506 BJ257506
	31	448.2	20.6	702	9	AI898064	AI898064 EST267507
c	32	447.2	20.6	819	14	CB627678	CB627678 OSIIEb02M
	33	444	20.4	558	14	CA007665	CA007665 HU08K12r
	34	443.4	20.4	768	14	CB644605	CB644605 OSJNEb05O
	35	440.4	20.2	667	14	CA501429	CA501429 WHE4033_E
	36	434	20.0	564	13	BU970618	BU970618 HB15C23r
	37	430.2	19.8	467	9	AW065933	AW065933 687003D03
	38	428.6	19.7	659	9	AW650691	AW650691 EST329145
	39	423	19.4	634	14	CD234077	CD234077 SS1_6_E12
	40	420.8	19.3	537	10	BF199845	BF199845 WHE0597_C
c	41	420.4	19.3	442	14	CA404257	CA404257 EL01N0514
	42	420.4	19.3	454	14	CA831042	CA831042 1117014G0
	43	414.4	19.1	733	13	BQ117168	BQ117168 EST602744
	44	414.2	19.0	530	13	BU974237	BU974237 HB27F01r
	45	408.2	18.8	576	14	CA501743	CA501743 WHE4038_B

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OM nucleic - nucleic search, using sw model

Run on: October 23, 2003, 16:56:57 ; Search time 7708 Seconds
                                             (without alignments)
                                             11543.648 Million cell updates/sec

Title: US-09-864-464-9
Perfect score: 2175
Sequence: 1 acttgagcctccaccttctc..........aattggtgcttttgatagcc 2175

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*
                 15: em_ba:*
                 16: em_fun:*
                 17: em_hum:*
                 18: em_in:*
                 19: em_mu:*
                 20: em_om:*
                 21: em_or:*
                 22: em_ov:*
                 23: em_pat:*
                 24: em_ph:*
                 25: em_pl:*
                 26: em_ro:*
                 27: em_sts:*

```
28:    em_un:*
29:    em_vi:*
30:    em_htg_hum:*
31:    em_htg_inv:*
32:    em_htg_other:*
33:    em_htg_mus:*
34:    em_htg_pln:*
35:    em_htg_rod:*
36:    em_htg_mam:*
37:    em_htg_vrt:*
38:    em_sy:*
39:    em_htgo_hum:*
40:    em_htgo_mus:*
41:    em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2175	100.0	2175	6	AR164421	AR164421 Sequence
	2	897.4	41.3	1938	8	BT002123	BT002123 Arabidops
	3	897.4	41.3	2083	8	AY099551	AY099551 Arabidops
	4	897.4	41.3	2193	8	AF125574	AF125574 Arabidops
	5	886.4	40.8	2143	6	AR164423	AR164423 Sequence
	6	745.6	34.3	2075	8	LELYSRSGN	X94451 L.esculentu
	7	539.4	24.8	1970	10	CLLYTRSY	Z31711 C.longicaud
	8	539.4	24.8	1997	9	BC004132	BC004132 Homo sapi
	9	539.2	24.8	2000	9	AF285758	AF285758 Homo sapi
	10	538	24.7	1970	9	HUMORFKG1S	D31890 Homo sapien
	11	538	24.7	1997	6	AX214528	AX214528 Sequence
	12	538	24.7	1997	9	D32053	D32053 Homo sapien
	13	537.8	24.7	2023	10	BC036289	BC036289 Mus muscu
	14	537.8	24.7	2146	10	BC035324	BC035324 Mus muscu
	15	537.8	24.7	2205	10	BC027356	BC027356 Mus muscu
	16	532.2	24.5	2036	5	BC046578	BC046578 Xenopus l
	17	527	24.2	2076	5	BC047965	BC047965 Xenopus l
	18	492.6	22.6	2205	3	AK114863	AK114863 Ciona int
	19	462.2	21.3	1896	3	AY089547	AY089547 Drosophil
	20	457.4	21.0	604	6	AR164422	AR164422 Sequence
	21	447.6	20.6	42696	2	AC012813	AC012813 Drosophil
c	22	447.6	20.6	159970	3	AC023702	AC023702 Drosophil
	23	447.6	20.6	161360	3	AC105292	AC105292 Drosophil
c	24	447.6	20.6	289621	3	AE003447	AE003447 Drosophil
	25	439	20.2	2480	8	SCKRS1	X56259 S.cerevisia
	26	437.4	20.1	2708	8	SCYDR037W	Z74333 S.cerevisia
	27	437.4	20.1	5180	8	YSCKRS1A	J04186 Yeast (S.ce
	28	437.4	20.1	24628	8	SC9673	Z68196 S.cerevisia
	29	435.8	20.0	1776	6	AX596068	AX596068 Sequence
c	30	425.4	19.6	32618	8	SPBC17G9	AL109846 S.pombe c
	31	423.8	19.5	107448	2	DMBR41K5	AL121843 Drosophil
	32	402.8	18.5	1991	6	AR071755	AR071755 Sequence
	33	400.8	18.4	1785	6	AX488967	AX488967 Sequence

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OM nucleic - nucleic search, using sw model

Run on: October 23, 2003, 16:54:42 ; Search time 563 Seconds
                                  (without alignments)
                                  10428.557 Million cell updates/sec

Title: US-09-864-464-9
Perfect score: 2175
Sequence: 1 acttgagcctccaccttctc.........aattggtgcttttgatagcc 2175

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_19Jun03:*
                  1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
                  2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
                  3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
                  4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
                  5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
                  6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
                  7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
                  8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
                  9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
                 10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
                 11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
                 12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
                 13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
                 14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
                 15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
                 16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
                 17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
                 18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
                 19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
                 20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
                 21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
                 22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
                 23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
                 24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
                 25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

     Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2175	100.0	2175	22	AAF87082	Corn lysyl-RNA syn
	2	897.4	41.3	1972	21	AAC51249	Arabidopsis thalia
	3	886.4	40.8	2143	22	AAF87084	Soybean lysyl-RNA
	4	641.4	29.5	1271	21	AAC38991	Arabidopsis thalia
	5	538	24.7	1997	22	AAH76461	cDNA corresponding
	6	538	24.7	1997	24	ABK83648	Human cDNA differe
	7	535.8	24.6	1639	24	ABS51524	Human cDNA encodin
	8	527.8	24.3	2169	25	ABX63347	Human cDNA #347 di
	9	464.6	21.4	2015	23	ABL04511	Drosophila melanog
	10	457.4	21.0	604	22	AAF87083	Rice lysyl-RNA syn
c	11	447.6	20.6	4361	23	ABL04510	Drosophila melanog
	12	402.8	18.5	1991	20	AAX76332	Pneumocystis carin
	13	400.8	18.4	1785	24	ABZ31980	Candida albicans e
	14	367.4	16.9	1818	25	ABT19056	Aspergillus fumiga
	15	367.4	16.9	1818	25	ABT20876	Aspergillus fumiga
	16	354.4	16.3	1903	25	ABT18462	Aspergillus fumiga
	17	354.4	16.3	1903	25	ABT20278	Aspergillus fumiga
	18	354.4	16.3	3903	25	ABT17868	Aspergillus fumiga
	19	354.4	16.3	3903	25	ABT19682	Aspergillus fumiga
	20	348	16.0	2128	20	AAX76373	P. carinii lysyl-t
	21	338.8	15.6	702	22	AAF87085	Wheat lysyl-RNA sy
	22	264	12.1	1487	23	AAS51633	Staphylococcus aur
	23	263.8	12.1	1521	24	ABN91007	Staphylococcus epi
	24	252.6	11.6	1503	24	ABN66580	Streptococcus poly
	25	249.2	11.5	1488	24	ABN70907	Streptococcus poly
	26	249.2	11.5	1599	24	ABN66579	Streptococcus poly
c	27	249.2	11.5	2155561	24	ABN71527	Streptococcus poly
	28	244.4	11.2	1497	23	AAS52822	Enterococcus faeca
	29	244.4	11.2	1500	23	AAS51370	Enterococcus faeca
	30	239	11.0	2944528	24	ABA03041	Listeria monocytog
	31	238.6	11.0	1518	23	AAS52719	E. coli DNA for ce
	32	237.6	10.9	6617	22	AAI97964	Lawsonia intracell
c	33	235.8	10.8	2365589	24	ABA90521	Genomic sequence o
c	34	234.6	10.8	4066	22	AAH54963	S. epidermidis gen
	35	232.8	10.7	45613	22	AAF28535	Genomic fragment #
	36	229.8	10.6	1163020	24	ABQ67197	Listeria innocua c
	37	229.8	10.6	3011208	24	ABQ69245	Listeria innocua D
	38	227.8	10.5	1473	25	ABX06381	S. pneumoniae type
	39	227.8	10.5	1491	23	AAS55666	Streptococcus pneu
	40	227.8	10.5	3232	19	AAV52277	Streptococcus pneu
	41	227.8	10.5	2162598	25	ABS56454	Streptococcus pneu
	42	226.2	10.4	1491	18	AAT92930	Streptococcus pneu
	43	226.2	10.4	1491	22	AAH42416	Nucleotide sequenc
	44	224.6	10.3	580073	18	AAT58840	Mycoplasma genital
	45	218	10.0	263	25	ABX84849	Corn ear-derived p

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: October 23, 2003, 18:21:52 ; Search time 152 Seconds
                                             (without alignments)
                                             6315.844 Million cell updates/sec

Title: US-09-864-464-9
Perfect score: 2175
Sequence: 1 acttgagcctccaccttctc..........aattggtgcttttgatagcc 2175

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query
   No.   Score Match Length DB   ID   Description
----
     1   2175 100.0   2175   3   US-09-357-251-9   Sequence 9, Appli
     2   886.4   40.8   2143   3   US-09-357-251-13   Sequence 13, Appl
     3   457.4   21.0   604   3   US-09-357-251-11   Sequence 11, Appl
     4   402.8   18.5   1991   2   US-08-415-593-40   Sequence 40, Appl
     5   348   16.0   2128   2   US-08-415-593-39   Sequence 39, Appl
     6   338.8   15.6   702   3   US-09-357-251-15   Sequence 15, Appl
     7   263.8   12.1   1521   4   US-09-134-001C-470   Sequence 470, App
     8   231.8   10.7   1566   4   US-09-328-352-1692   Sequence 1692, Ap
     9   231.6   10.6   1290   4   US-09-107-532A-3187   Sequence 3187, Ap
    10   227.8   10.5   3232   4   US-08-961-527-144   Sequence 144, App
    11   226.2   10.4   1491   3   US-08-833-876-1   Sequence 1, Appli

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OM nucleic - nucleic search, using sw model

Run on: October 23, 2003, 20:48:08 ; Search time 575 Seconds
                                          (without alignments)
                                          10144.203 Million cell updates/sec

Title: US-09-864-464-9
Perfect score: 2175
Sequence: 1 acttgagcctccaccttctc..........aattggtgcttttgatagcc 2175

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                 1:   /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                 2:   /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                 3:   /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                 4:   /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
                 5:   /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                 6:   /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
                 7:   /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                 8:   /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                 9:   /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
                 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
                 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
                 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                 15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                 16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
                 17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	535.8	24.6	1639	14	US-10-043-487-104	Sequence 104, App
2	527.8	24.3	2169	13	US-10-044-090-347	Sequence 347, App
3	400.8	18.4	1785	12	US-10-032-585-6267	Sequence 6267, Ap
4	367.4	16.9	1818	14	US-10-128-714-2226	Sequence 2226, Ap
5	367.4	16.9	1818	14	US-10-128-714-7226	Sequence 7226, Ap
6	354.4	16.3	1903	14	US-10-128-714-1226	Sequence 1226, Ap
7	354.4	16.3	1903	14	US-10-128-714-6226	Sequence 6226, Ap
8	354.4	16.3	3903	14	US-10-128-714-226	Sequence 226, App
9	354.4	16.3	3903	14	US-10-128-714-5226	Sequence 5226, Ap
10	264	12.1	1487	9	US-09-815-242-4215	Sequence 4215, Ap
11	244.4	11.2	1497	9	US-09-815-242-6459	Sequence 6459, Ap
12	244.4	11.2	1500	9	US-09-815-242-3952	Sequence 3952, Ap
13	238.6	11.0	1518	9	US-09-815-242-6356	Sequence 6356, Ap
14	237.6	10.9	6617	14	US-10-210-296-1	Sequence 1, Appli
15	232.4	10.7	234	9	US-09-923-876-18	Sequence 18, Appl
16	227.8	10.5	1491	9	US-09-815-242-9303	Sequence 9303, Ap
17	224.6	10.3	580073	12	US-10-205-220-1	Sequence 1, Appli
18	224	10.3	38459	12	US-09-960-858-3	Sequence 3, Appli
19	224	10.3	38459	12	US-09-960-870-3	Sequence 3, Appli
20	216.6	10.0	1506	9	US-09-815-242-7203	Sequence 7203, Ap
21	215.6	9.9	565	14	US-10-066-543-2312	Sequence 2312, Ap
22	214.2	9.8	873	9	US-09-815-242-8618	Sequence 8618, Ap
c 23	212	9.7	1830121	14	US-10-329-960-1	Sequence 1, Appli
24	210.2	9.7	1509	9	US-09-815-242-7108	Sequence 7108, Ap
25	205.8	9.5	484	11	US-09-918-995-25525	Sequence 25525, A
26	204.6	9.4	1518	9	US-09-741-669-159	Sequence 159, App
27	204.6	9.4	1518	9	US-09-815-242-6188	Sequence 6188, Ap
28	198.8	9.1	554	10	US-09-796-692-5756	Sequence 5756, Ap
29	198.8	9.1	554	14	US-10-040-862-5756	Sequence 5756, Ap
c 30	198.4	9.1	680	9	US-09-835-992A-39	Sequence 39, Appl
31	192.2	8.8	640681	10	US-09-790-988-1	Sequence 1, Appli
32	191.4	8.8	987	9	US-09-815-242-9774	Sequence 9774, Ap
c 33	179.2	8.2	537	14	US-10-066-543-163	Sequence 163, App
34	169	7.8	975	10	US-09-974-300-1181	Sequence 1181, Ap
35	167.4	7.7	347	10	US-09-920-300A-1236	Sequence 1236, Ap
36	167.4	7.7	347	12	US-10-099-926-1236	Sequence 1236, Ap
37	167.4	7.7	347	13	US-10-033-528-1236	Sequence 1236, Ap
c 38	167.4	7.7	873	8	US-08-781-986A-196	Sequence 196, App
39	152.2	7.0	1506	9	US-09-815-242-7845	Sequence 7845, Ap
40	147.4	6.8	432	11	US-09-918-995-16229	Sequence 16229, A
41	144.8	6.7	648	10	US-09-974-300-5592	Sequence 5592, Ap
42	144.6	6.6	497	11	US-09-918-995-20671	Sequence 20671, A
43	128	5.9	128	9	US-09-294-093B-1888	Sequence 1888, Ap
44	125.8	5.8	1518	10	US-09-712-363-129	Sequence 129, App
45	117.2	5.4	420	9	US-09-815-242-8050	Sequence 8050, Ap

ALIGNMENTS

RESULT 1
US-10-043-487-104

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 23, 2003, 21:56:34 ; Search time 409 Seconds
                                              (without alignments)
                                              4184.459 Million cell updates/sec

Title: US-09-864-464-10
Perfect score: 3331
Sequence: 1 LSLHLLRVSPSSPFSFRSPL..........LTDSQNIKEVLLFPAMKPQE 634

Scoring table: BLOSUM62
                   Xgapop 10.0 , Xgapext 0.5
                   Ygapop 10.0 , Ygapext 0.5
                   Fgapop 6.0 , Fgapext 7.0
                   Delop   6.0 , Delext   7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US09864464/runat_22102003_171604_3925/app_query.fasta_1.
775
-DB=N_Geneseq_19Jun03 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09864464_@CGN_1_1_490_@runat_22102003_171604_3925 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   N_Geneseq_19Jun03:*
                   1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
                   2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
                   3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
                   4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
                   5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
                   6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
                   7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
                   8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
                   9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
                   10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*

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11:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
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19:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
25:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	3331	100.0	2175	22	AAF87082	Corn lysyl-RNA syn
	2	2336	70.1	2143	22	AAF87084	Soybean lysyl-RNA
	3	2287.5	68.7	1972	21	AAC51249	Arabidopsis thalia
	4	1778	53.4	1997	22	AAH76461	cDNA corresponding
	5	1778	53.4	1997	24	ABK83648	Human cDNA differe
	6	1752.5	52.6	2015	23	ABL04511	Drosophila melanog
	7	1742	52.3	2169	25	ABX63347	Human cDNA #347 di
	8	1719.5	51.6	1639	24	ABS51524	Human cDNA encodin
c	9	1674.5	50.3	4361	23	ABL04510	Drosophila melanog
	10	1655	49.7	1271	21	AAC38991	Arabidopsis thalia
	11	1574	47.3	1785	24	ABZ31980	Candida albicans e
	12	1571	47.2	1991	20	AAX76332	Pneumocystis carin
	13	1542.5	46.3	1818	25	ABT19056	Aspergillus fumiga
	14	1542.5	46.3	1818	25	ABT20876	Aspergillus fumiga
	15	1527	45.8	2128	20	AAX76373	P. carinii lysyl-t
	16	1510.5	45.3	1903	25	ABT18462	Aspergillus fumiga
	17	1510.5	45.3	1903	25	ABT20278	Aspergillus fumiga
	18	1510.5	45.3	3903	25	ABT17868	Aspergillus fumiga
	19	1510.5	45.3	3903	25	ABT19682	Aspergillus fumiga
	20	986	29.6	1163020	24	ABQ67197	Listeria innocua c
	21	986	29.6	3011208	24	ABQ69245	Listeria innocua D
	22	983	29.5	2944528	24	ABA03041	Listeria monocytog
	23	976.5	29.3	1521	24	ABN91007	Staphylococcus epi
	24	957	28.7	1487	23	AAS51633	Staphylococcus aur
c	25	956.5	28.7	2365589	24	ABA90521	Genomic sequence o
	26	947	28.4	1506	23	AAS53566	Helicobacter pylor
	27	946.5	28.4	1692	19	AAV53138	Helicobacter lysyl
	28	939	28.2	3232	19	AAV52277	Streptococcus pneu
	29	939	28.2	2162598	25	ABS56454	Streptococcus pneu
	30	937.5	28.1	1473	25	ABX06381	S. pneumoniae type
	31	937.5	28.1	1491	18	AAT92930	Streptococcus pneu
	32	937.5	28.1	1491	22	AAH42416	Nucleotide sequenc

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 23, 2003, 23:47:49 ; Search time 112 Seconds
                                            (without alignments)
                                            2498.544 Million cell updates/sec

Title: US-09-864-464-10
Perfect score: 3331
Sequence: 1 LSLHLLRVSPSSPFSFRSPL..........LTDSQNIKEVLLFPAMKPQE 634

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US09864464/runat_22102003_171605_3965/app_query.fasta_1.
775
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09864464_@CGN_1_1_103_@runat_22102003_171605_3965 -NCPU=6 -TCPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES 0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	3331	100.0	2175	3	US-09-357-251-9	Sequence 9, Appli
	2	2336	70.1	2143	3	US-09-357-251-13	Sequence 13, Appl
	3	1571	47.2	1991	2	US-08-415-593-40	Sequence 40, Appl
	4	1527	45.8	2128	2	US-08-415-593-39	Sequence 39, Appl
	5	976.5	29.3	1521	4	US-09-134-001C-470	Sequence 470, App
	6	946.5	28.4	1692	1	US-08-451-715A-9	Sequence 9, Appli
	7	939	28.2	3232	4	US-08-961-527-144	Sequence 144, App
	8	937.5	28.1	1491	3	US-08-833-876-1	Sequence 1, Appli
	9	937.5	28.1	1491	4	US-09-483-054-1	Sequence 1, Appli
	10	929	27.9	604	3	US-09-357-251-11	Sequence 11, Appl
	11	926	27.8	1566	4	US-09-328-352-1692	Sequence 1692, Ap
	12	893.5	26.8	1290	4	US-09-107-532A-3187	Sequence 3187, Ap
c	13	877.5	26.3	1770	4	US-09-252-991A-1522	Sequence 1522, Ap
	14	877	26.3	1524	4	US-09-252-991A-1651	Sequence 1651, Ap
c	15	860.5	25.8	1830121	4	US-09-557-884-1	Sequence 1, Appli
c	16	860.5	25.8	1830121	4	US-09-643-990A-1	Sequence 1, Appli
	17	822	24.7	580073	4	US-08-545-528D-1	Sequence 1, Appli
	18	785	23.6	1581	2	US-08-898-780A-1	Sequence 1, Appli
	19	785	23.6	1581	3	US-09-270-917-1	Sequence 1, Appli
c	20	753	22.6	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	21	753	22.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	22	741.5	22.3	3072	4	US-09-221-017B-337	Sequence 337, App
	23	725	21.8	1230025	4	US-09-198-452A-1	Sequence 1, Appli
	24	708	21.3	702	3	US-09-357-251-15	Sequence 15, Appl
c	25	518	15.6	680	3	US-08-896-164-39	Sequence 39, Appl
	26	447	13.4	813	4	US-09-252-991A-1600	Sequence 1600, Ap
	27	424.5	12.7	894	4	US-09-252-991A-1599	Sequence 1599, Ap
	28	387	11.6	263	4	US-09-313-294A-3309	Sequence 3309, Ap
c	29	355.5	10.7	537	4	US-09-107-532A-108	Sequence 108, App
	30	325	9.8	1830121	4	US-09-557-884-1	Sequence 1, Appli
	31	325	9.8	1830121	4	US-09-643-990A-1	Sequence 1, Appli
	32	323	9.7	287	2	US-08-415-593-34	Sequence 34, Appl
c	33	316	9.5	1803	4	US-09-252-991A-12466	Sequence 12466, A
	34	316	9.5	1971	4	US-09-252-991A-13004	Sequence 13004, A
c	35	315	9.5	1664976	4	US-08-916-421B-1	Sequence 1, Appli
	36	314.5	9.4	1002	4	US-09-328-352-3015	Sequence 3015, Ap
	37	314.5	9.4	2007	4	US-08-829-402-1	Sequence 1, Appli
	38	310.5	9.3	1782	4	US-09-134-001C-755	Sequence 755, App
	39	276.5	8.3	1362	4	US-09-328-352-1146	Sequence 1146, Ap
c	40	270.5	8.1	13104	4	US-08-961-527-34	Sequence 34, Appl
	41	269.5	8.1	1770	4	US-09-107-532A-2432	Sequence 2432, Ap
	42	269.5	8.1	1948	3	US-09-352-990-1	Sequence 1, Appli
	43	268.5	8.1	1764	1	US-08-844-280-1	Sequence 1, Appli
	44	268.5	8.1	1764	3	US-09-006-726-1	Sequence 1, Appli
	45	261	7.8	392	3	US-08-833-876-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-357-251-9

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2003, 01:37:25 ; Search time 414 Seconds
                                              (without alignments)
                                              4106.912 Million cell updates/sec

Title: US-09-864-464-10
Perfect score: 3331
Sequence: 1 LSLHLLRVSPSSPFSFRSPL.........LTDSQNIKEVLLFPAMKPQE 634

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US09864464/runat_22102003_171606_4046/app_query.fasta 1.
775
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09864464_@CGN_1_1_107_@runat_22102003_171606_4046
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_NA:*
                 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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                 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
                 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
                 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

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11:  /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12:  /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13:  /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14:  /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15:  /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
16:  /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
17:  /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1742	52.3	2169	13	US-10-044-090-347	Sequence 347, App
	2	1719.5	51.6	1639	14	US-10-043-487-104	Sequence 104, App
	3	1574	47.3	1785	12	US-10-032-585-6267	Sequence 6267, Ap
	4	1542.5	46.3	1818	14	US-10-128-714-2226	Sequence 2226, Ap
	5	1542.5	46.3	1818	14	US-10-128-714-7226	Sequence 7226, Ap
	6	1510.5	45.3	1903	14	US-10-128-714-1226	Sequence 1226, Ap
	7	1510.5	45.3	1903	14	US-10-128-714-6226	Sequence 6226, Ap
	8	1510.5	45.3	3903	14	US-10-128-714-226	Sequence 226, App
	9	1510.5	45.3	3903	14	US-10-128-714-5226	Sequence 5226, Ap
	10	957	28.7	1487	9	US-09-815-242-4215	Sequence 4215, Ap
	11	947	28.4	1506	9	US-09-815-242-7203	Sequence 7203, Ap
	12	937.5	28.1	1491	9	US-09-815-242-9303	Sequence 9303, Ap
	13	933	28.0	1497	9	US-09-815-242-6459	Sequence 6459, Ap
	14	933	28.0	1500	9	US-09-815-242-3952	Sequence 3952, Ap
	15	925.5	27.8	6617	14	US-10-210-296-1	Sequence 1, Appli
	16	917.5	27.5	1518	9	US-09-815-242-6356	Sequence 6356, Ap
	17	906	27.2	1518	9	US-09-741-669-159	Sequence 159, App
	18	906	27.2	1518	9	US-09-815-242-6188	Sequence 6188, Ap
	19	876	26.3	1506	9	US-09-815-242-7845	Sequence 7845, Ap
	20	868	26.1	640681	10	US-09-790-988-1	Sequence 1, Appli
	21	860.5	25.8	1509	9	US-09-815-242-7108	Sequence 7108, Ap
c	22	860.5	25.8	1830121	14	US-10-329-960-1	Sequence 1, Appli
	23	822	24.7	38459	12	US-09-960-858-3	Sequence 3, Appli
	24	822	24.7	38459	12	US-09-960-870-3	Sequence 3, Appli
	25	822	24.7	580073	12	US-10-205-220-1	Sequence 1, Appli
c	26	790.5	23.7	3309400	10	US-09-738-626-1	Sequence 1, Appli
	27	782.5	23.5	1578	10	US-09-738-626-2954	Sequence 2954, Ap
	28	751	22.5	1518	10	US-09-712-363-129	Sequence 129, App
	29	734	22.0	3279	14	US-10-156-761-7275	Sequence 7275, Ap
	30	734	22.0	9025608	14	US-10-156-761-1	Sequence 1, Appli
	31	732	22.0	987	9	US-09-815-242-9774	Sequence 9774, Ap
	32	706.5	21.2	873	9	US-09-815-242-8618	Sequence 8618, Ap
	33	693	20.8	565	14	US-10-066-543-2312	Sequence 2312, Ap
	34	666.5	20.0	975	10	US-09-974-300-1181	Sequence 1181, Ap
	35	660	19.8	554	10	US-09-796-692-5756	Sequence 5756, Ap
	36	660	19.8	554	14	US-10-040-862-5756	Sequence 5756, Ap
c	37	599	18.0	537	14	US-10-066-543-163	Sequence 163, App
	38	569	17.1	484	11	US-09-918-995-25525	Sequence 25525, A
c	39	556.5	16.7	873	8	US-08-781-986A-196	Sequence 196, App
c	40	518	15.6	680	9	US-09-835-992A-39	Sequence 39, Appl

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 23, 2003, 23:39:54 ; Search time 2884 Seconds
                                             (without alignments)
                                             5342.940 Million cell updates/sec

Title: US-09-864-464-10
Perfect score: 3331
Sequence: 1 LSLHLLRVSPSSPFSFRSPL..........LTDSQNIKEVLLFPAMKPQE 634

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US09864464/runat_22102003_171605_3947/app_query.fasta_1.
775
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09864464_@CGN_1_1_3549_@runat_22102003_171605_3947 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   EST:*
                 1: em_estba:*
                 2: em_esthum:*
                 3: em_estin:*
                 4: em_estmu:*
                 5: em_estov:*
                 6: em_estpl:*
                 7: em_estro:*
                 8: em_htc:*
                 9: gb_est1:*
                 10: gb_est2:*

```
11:  gb_htc:*
12:  gb_est3:*
13:  gb_est4:*
14:  gb_est5:*
15:  em_estfun:*
16:  em_estom:*
17:  em_gss_hum:*
18:  em_gss_inv:*
19:  em_gss_pln:*
20:  em_gss_vrt:*
21:  em_gss_fun:*
22:  em_gss_mam:*
23:  em_gss_mus:*
24:  em_gss_pro:*
25:  em_gss_rod:*
26:  em_gss_phg:*
27:  em_gss_vrl:*
28:  gb_gss1:*
29:  gb_gss2:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	3331	100.0	2220	11	AY103979	AY103979 Zea mays
	2	1784	53.6	1963	11	AK089053	AK089053 Mus muscu
	3	1782	53.5	1963	11	AK090203	AK090203 Mus muscu
	4	1775.5	53.3	1960	11	BC013246	BC013246 Homo sapi
	5	1331	40.0	776	14	CD432929	CD432929 EL01N0302
	6	1314	39.4	771	14	CD445806	CD445806 EL01T0203
	7	1151.5	34.6	860	14	CB627677	CB627677 OSIIEb02M
	8	1138	34.2	702	9	AI898064	AI898064 EST267507
	9	1093	32.8	663	12	BJ549326	BJ549326 BJ549326
	10	1078	32.4	684	10	BE585724	BE585724 Est#1SP6_
	11	1067	32.0	733	13	BQ117168	BQ117168 EST602744
	12	1066	32.0	882	13	BQ215534	BQ215534 AGENCOURT
	13	1053	31.6	631	9	AW066125	AW066125 687006E08
	14	1052	31.6	881	13	BU176615	BU176615 AGENCOURT
	15	1049	31.5	882	12	BI905374	BI905374 603167411
	16	1037	31.1	659	9	AW650691	AW650691 EST329145
	17	1017	30.5	601	14	CD443593	CD443593 EL01N0428
	18	1011	30.4	932	13	BX327446	BX327446 BX327446
	19	1008.5	30.3	672	9	AW685961	AW685961 NF036H08N
c	20	1004.5	30.2	1201	9	AL567684	AL567684 AL567684
	21	999	30.0	991	29	CNS06YSR	AL421441 T3 end of
	22	998	30.0	942	14	CB183903	CB183903 AGENCOURT
	23	997.5	29.9	915	13	BX327445	BX327445 BX327445
c	24	997	29.9	1201	9	AL581487	AL581487 AL581487
	25	994	29.8	632	9	AV833455	AV833455 AV833455
	26	991	29.8	650	14	CA741660	CA741660 wialc.pk0
	27	988	29.7	929	14	CB209380	CB209380 AGENCOURT
	28	984	29.5	919	10	BG682242	BG682242 602629550

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 23, 2003, 21:59:29 ; Search time 5432 Seconds
                                              (without alignments)
                                              4774.798 Million cell updates/sec

Title: US-09-864-464-10
Perfect score: 3331
Sequence: 1 LSLHLLRVSPSSPFSFRSPL..........LTDSQNIKEVLLFPAMKPQE 634

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US09864464/runat_22102003_171604_3935/app_query.fasta_1.
775
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09864464_@CGN_1_1_4958_@runat_22102003_171604_3935 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT 30 -THREADS 1 -XGAPOP 10 -XGAPEXT 0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*

```
11:  gb_sts:*
12:  gb_sy:*
13:  gb_un:*
14:  gb_vi:*
15:  em_ba:*
16:  em_fun:*
17:  em_hum:*
18:  em_in:*
19:  em_mu:*
20:  em_om:*
21:  em_or:*
22:  em_ov:*
23:  em_pat:*
24:  em_ph:*
25:  em_pl:*
26:  em_ro:*
27:  em_sts:*
28:  em_un:*
29:  em_vi:*
30:  em_htg_hum:*
31:  em_htg_inv:*
32:  em_htg_other:*
33:  em_htg_mus:*
34:  em_htg_pln:*
35:  em_htg_rod:*
36:  em_htg_mam:*
37:  em_htg_vrt:*
38:  em_sy:*
39:  em_htgo_hum:*
40:  em_htgo_mus:*
41:  em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	3331	100.0	2175	6	AR164421	AR164421 Sequence
	2	2336	70.1	2143	6	AR164423	AR164423 Sequence
	3	2287.5	68.7	1938	8	BT002123	BT002123 Arabidops
	4	2287.5	68.7	2083	8	AY099551	AY099551 Arabidops
	5	2287.5	68.7	2193	8	AF125574	AF125574 Arabidops
	6	2084	62.6	2075	8	LELYSRSGN	X94451 L.esculentu
c	7	1854	55.7	45173	8	ATAC009918	AC009918 Arabidops
c	8	1854	55.7	100835	8	ATAC016795	AC016795 Arabidops
	9	1790.5	53.8	2205	10	BC027356	BC027356 Mus muscu
	10	1789	53.7	2023	10	BC036289	BC036289 Mus muscu
	11	1781.5	53.5	1970	10	CLLYTRSY	Z31711 C.longicaud
	12	1781.5	53.5	1997	9	BC004132	BC004132 Homo sapi
	13	1780.5	53.5	2146	10	BC035324	BC035324 Mus muscu
	14	1778	53.4	1997	6	AX214528	AX214528 Sequence
	15	1778	53.4	1997	9	D32053	D32053 Homo sapien
	16	1775.5	53.3	1970	9	HUMORFKG1S	D31890 Homo sapien